



## SEQUENCE LISTING

<110> Caput, Daniel  
Ferrara, Pascual  
Laurent, Patrick  
Vita, Natalio

<120> IL-13 RECEPTOR

<130> IVD924

<140> 09/077,817

<141> 1998-09-14

<150> PCT/FR96/01756

<151> 1996-11-07

<160> 15

<170> PatentIn Ver. 2.0

<210> 1

<211> 1298

<212> DNA

<213> Homo sapiens

<400> 1

ggcgcctgtc ggcgggggaga gaggcaatat caagggtttta aatctcggag aaatggcttt	60
cgtttgcttg gctatcggat gcttatatac ctttctgata agcacaacat ttggctgtac	120
ttcatcttca gacaccgaga taaaagttaa cctcctcag gattttgaga tagtggatcc	180
cggatactta ggttatctct atttgcaatg gcaacccccca ctgtctctgg atcattttta	240
ggaatgcaca gtggaatatg aactaaaata ccgaaacatt ggtagtgaaa catggaagac	300
catcattact aagaatctac attacaaaga tgggtttgat cttacaagg gcattgaagc	360
gaagatacac acgcttttac catggcaatg cacaatgga tcagaagttc aaagttcctg	420
ggcagaaact acttattgga taccaccaca aggaattcca gaaactaaag ttcaggatat	480
ggattgcgta tattacaatt ggcaatatct actctgttct tggaaacctg gcataggtgt	540
acttcttgat accaattaca acttggtttta ctggtatgag ggcttggatc atgcattaca	600
gtgtgttgat tacatcaagg ctgatggaca aaatatagga tgcagatttc cctatttgga	660
ggcatcagac tataaagatt tctatatattg tgtaaatgga tcatcagaga acaagcctat	720
cagatccagt tatttcactt ttcagcttca aaatatagtt aaacctttgc cgccagtcta	780
tcttactttt actcgggaga gttcatgtga aattaagctg aaatggagca tacctttggg	840
acctattcca gcaagggtgtt ttgattatga aattgagatc agagaagatg atactacctt	900

```

ggtgactgct acagttgaaa atgaaacata caccttgaaa acaacaaatg aaacccgaca      960
attatgcttt gtagtaagaa gcaaagtgaa tattttattgc tcagatgacg gaatttgagg      1020
tgagtggagt gataaacaat gctgggaagg tgaagaccta tcgaagaaaa ctttgctacg      1080
tttctggcta ccatttggtt tcatcttaat attagttata tttgtaaccg gtctgctttt      1140
gcgtaagcca aacacctacc caaaaatgat tccagaatth ttctgtgata catgaagact      1200
ttccatatca agagacatgg tattgactca acagtttcca gtcatggcca aatgttcaat      1260
atgagtctca ataaactgaa tttttcttgc gaatgttg      1298

```

<210> 2

<211> 380

<212> PRT 3

<213> Homo sapiens

<400> 2

```

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
 1          5          10          15
Ser Thr Thr Phe Gly Cys Thr Ser Ser Asp Thr Glu Ile Lys Val
 20          25          30
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
 35          40          45
Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
 50          55          60
Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
 65          70          75          80
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 85          90          95
Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100          105          110
Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
115          120          125
Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
130          135          140
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
145          150          155          160
Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
165          170          175
Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
180          185          190
Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
195          200          205
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
210          215          220
Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
225          230          235          240
Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
245          250          255
Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr

```

	260		265		270
Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val					
275		280		285	
Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu					
290		295		300	
Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly					
305		310		315	320
Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu					
	325		330		335
Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu					
	340		345		350
Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr					
	355		360		365
Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr					
	370		375		380

&lt;210&gt; 3

&lt;211&gt; 4009

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

tcagcccggc cgggctccga ggcgagaggc tgcattggagt ggccggcgcg gctctgcggg	60
ctgtgggccc tgctgctctg cgccggcgcc gggggcgggg gcggggcgcc cgcgccctacg	120
gaaactcagc cacctgtgac aaatttgagt gtctctgttg aaaacctctg cacagtaata	180
tggacatgga atccacccga gggagccagc tcaaattgta gtctatggta ttttagtcat	240
tttgggcgaca aacaagataa gaaaatagct ccggaaactc gtcgttcaat agaagtaccc	300
ctgaatgaga ggatttgtct gcaagtgggg tcccagtgtg gcaccaatga gaggagaag	360
cctagcattt tgggtgaaaa atgcatctca ccccgagaag gtgatcctga gtctgctgtg	420
actgagcttc aatgcatttg gcacaacctg agctacatga agtggttcttg gctccctgga	480
aggaatacca gtcccgacac taactatact ctctactatt ggcacagaag cctggaaaaa	540
attcatcaat gtgaaaacat ctttagagaa ggccaatact ttggttggtc ctttgatctg	600
accaaagtga aggattccag ttttgaacaa cacagtgtcc aaataatggt caaggataat	660
gcaggaaaaa ttaaaccatc cttcaatata gtgcctttaa cttcccggtg gaaacctgat	720
cctccacata ttaaaaacct ctccttcac aatgatgacc tatatgtgca atgggagaat	780
ccacagaatt ttattagcag atgcctattt tatgaagtag aagtcaataa cagccaaact	840
gagacacata atgttttcta cgtccaagag gctaaatgtg agaatccaga atttgagaga	900
aatgtggaga atacatcttg tttcatggtc cctggtgttc ttctgatac tttgaacaca	960
gtcagaataa gaggcaaac aaataagtta tgctatgagg atgacaaact ctggagtaat	1020

tggagccaag aaatgagtat aggtaagaag cgcaattcca cactctacat aaccatgtta	1080
ctcattgttc cagtcacgt cgcaggtgca atcatagtag tcttgcttta cctaaaaagg	1140
ctcaagatta ttatatccc tccaattcct gatcctggca agatttttaa agaaatgttt	1200
ggagaccaga atgatgatac tctgcactgg aagaagtacg acatctatga gaagcaaacc	1260
aaggaggaaa ccgactctgt agtgctgata gaaaacctga agaaagcctc tcagtgatgg	1320
agataattta tttttacctt cactgtgacc ttgagaagat tcttcccatt ctccatttgt	1380
tatctgggaa cttattaaat ggaaactgaa actactgcac catttaaaaa caggcagctc	1440
ataagagcca caggtcttta tgttgagtcg cgcaccgaaa aactaaaaat aatgggcgct	1500
ttggagaaga gtgtggagtc attctcattg aattataaaa gccagcaggc ttcaaactag	1560
gggacaaagc aaaaagtgat gatagtgtg gagttaatct tatcaagagt tgtgacaact	1620
tctgagggga tctatacttg ctttgtgttc tttgtgtcaa catgaacaaa ttttatttgt	1680
aggggaactc atttggggtg caaatgctaa tgtcaaacctt gagtcacaaa gaacatgtag	1740
aaaacaaaat ggataaaatc tgatatgtat tgtttgggat cctattgaac catgtttgtg	1800
gctattaaaa ctcttttaac agtctgggct ggggccggtg gctcacgcct gtaatcccag	1860
caatttggga gtccgaggcg ggcggatcac tcgaggctcag gagttccaga ccagcctgac	1920
caaaatgggtg aaacctcctc tctactaaaa ctacaaaaat taactgggtg tgggtggcgcg	1980
tgctgtaat cccagctact cggaagctg aggcagggtga attgtttgaa cctgggaggt	2040
ggaggttgca gtgagcagag atcacaccac tgcactctag cctgggtgac agagcaagac	2100
tctgtctaaa aaacaaaaca aaacaaaaca aaacaaaaaa acctcttaat attctggagt	2160
catcattccc ttcgacagca ttttcctctg ctttgaaagc cccagaaatc agtgttggcc	2220
atgatgacaa ctacagaaaa accagaggca gcttctttgc caagacctt caaagccatt	2280
ttaggctgtt aggggcagtg gaggtagaat gactccttg gtattagagt ttcaaccatg	2340
aagtctctaa caatgtattt tcttcacctc tgctactcaa gtagcattta ctgtgtcttt	2400
ggtttgtgct agggccccgg gtgtgaagca cagaccctt ccaggggttt acagtctatt	2460
tgagactcct cagttcttgc cacttttttt tttaatctcc accagtcatt tttcagacct	2520
tttaactcct caattccaac actgatttcc ccttttgcat tctcctcct tcccttctt	2580
gtagcctttt gactttcatt ggaaattagg atgtaaatct gctcaggaga cctggaggag	2640
cagaggataa ttagcatctc aggttaagtg tgagtaatct gagaaacaat gactaattct	2700

```

tgcataat ttt gtaacttcca tgtgaggggt ttcagcattg atatttgtgc attttctaaa 2760
cagagatgag gtgggtatctt cacgtagaac attgggtattc gcttgagaaa aaaagaatag 2820
ttgaacctat ttctctttct ttacaagatg ggtccaggat tctctttttc tctgccataa 2880
atgattaatt aaatagcttt tgtgtcttac attggtagcc agccagccaa ggctctgttt 2940
atgcttttgg ggggcatata ttgggttcca ttctcaccta tccacacaac atatccgtat 3000
atatccctc tactcttact tcccccaa ttaaagaagt atgggaaatg agaggcattt 3060
ccccacccc atttctctcc tcacacacag actcatatta ctggtaggaa cttgagaact 3120
ttattttcaa gttgttcaaa catttaccaa tcatattaat acaatgatgc tatttgcaat 3180
tctgtctcct aggggagggg agataagaaa cctcactct ctacagggtt gggtagaagt 3240
ggcaacctgc ttccatggcc gtgtagaagc atgggtgccct ggcttctctg aggaagctgg 3300
ggttcatgac aatggcagat gtaaagttat tcttgaagtc agattgaggc tgggagacag 3360
ccgtagtaga tgttctactt tgttctgctg ttctctagaa agaataattg gttttcctgt 3420
ataggaatga gattaattcc tttccaggta tttataatt ctgggaagca aaacccatgc 3480
ctccccctag ccatttttac tgttatccta tttagatggc catgaagagg atgctgtgaa 3540
attcccaaca aacattgatg ctgacagtca tgcagtctgg gagtggggaa gtgatctttt 3600
gttcccatcc tcttctttta gcagtaaaat agctgagggg aaaggaggagg aaaaggaagt 3660
tatgggaata cctgtgggtg ttgtgatccc taggtcttgg gagctcttgg aggtgtctgt 3720
atcagtggat ttcccatccc ctgtgggaaa ttagtaggct catttactgt tttaggctca 3780
gcctatgtgg attttttcct aacataccta agcaaaccga gtgtcaggat ggtaattctt 3840
attctttcgt tcagttaagt ttttccttc atctgggcac tgaagggata tgtgaaacaa 3900
tgттаacatt tttggtagtc ttcaaccagg gattgtttct gtttaacttc ttataggaaa 3960
gcttgagtaa aataaatatt gtctttttgt atgtcaccca aaaaaaaaaa 4009

```

<210> 4

<211> 427

<212> PRT 3

<213> Homo sapiens

<400> 4

```

Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
1           5           10          15
Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln
          20          25          30

```

Pro	Pro	Val	Thr	Asn	Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Val
		35					40					45			
Ile	Trp	Thr	Trp	Asn	Pro	Pro	Glu	Gly	Ala	Ser	Ser	Asn	Cys	Ser	Leu
	50					55					60				
Trp	Tyr	Phe	Ser	His	Phe	Gly	Asp	Lys	Gln	Asp	Lys	Lys	Ile	Ala	Pro
	65				70					75					80
Glu	Thr	Arg	Arg	Ser	Ile	Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu
				85					90					95	
Gln	Val	Gly	Ser	Gln	Cys	Ser	Thr	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Ile
			100					105					110		
Leu	Val	Glu	Lys	Cys	Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala
		115					120					125			
Val	Thr	Glu	Leu	Gln	Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys
	130					135					140				
Ser	Trp	Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu
	145				150					155					160
Tyr	Tyr	Trp	His	Arg	Ser	Leu	Glu	Lys	Ile	His	Gln	Cys	Glu	Asn	Ile
				165					170					175	
Phe	Arg	Glu	Gly	Gln	Tyr	Phe	Gly	Cys	Ser	Phe	Asp	Leu	Thr	Lys	Val
			180					185					190		
Lys	Asp	Ser	Ser	Phe	Glu	Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp
		195					200					205			
Asn	Ala	Gly	Lys	Ile	Lys	Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser
	210					215					220				
Arg	Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	Asn	Leu	Ser	Phe	His	Asn
	225				230					235					240
Asp	Asp	Leu	Tyr	Val	Gln	Trp	Glu	Asn	Pro	Gln	Asn	Phe	Ile	Ser	Arg
				245					250					255	
Cys	Leu	Phe	Tyr	Glu	Val	Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	His
			260					265					270		
Asn	Val	Phe	Tyr	Val	Gln	Glu	Ala	Lys	Cys	Glu	Asn	Pro	Glu	Phe	Glu
		275					280					285			
Arg	Asn	Val	Glu	Asn	Thr	Ser	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro
	290					295					300				
Asp	Thr	Leu	Asn	Thr	Val	Arg	Ile	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys
	305				310					315					320
Tyr	Glu	Asp	Asp	Lys	Leu	Trp	Ser	Asn	Trp	Ser	Gln	Glu	Met	Ser	Ile
				325					330					335	
Gly	Lys	Lys	Arg	Asn	Ser	Thr	Leu	Tyr	Ile	Thr	Met	Leu	Leu	Ile	Val
			340					345					350		
Pro	Val	Ile	Val	Ala	Gly	Ala	Ile	Ile	Val	Leu	Leu	Leu	Tyr	Leu	Lys
		355					360					365			
Arg	Leu	Lys	Ile	Ile	Ile	Phe	Pro	Pro	Ile	Pro	Asp	Pro	Gly	Lys	Ile
	370					375					380				
Phe	Lys	Glu	Met	Phe	Gly	Asp	Gln	Asn	Asp	Asp	Thr	Leu	His	Trp	Lys
	385				390					395					400
Lys	Tyr	Asp	Ile	Tyr	Glu	Lys	Gln	Thr	Lys	Glu	Glu	Thr	Asp	Ser	Val
				405					410					415	
Val	Leu	Ile	Glu	Asn	Leu	Lys	Lys	Ala	Ser	Gln					
			420					425							

&lt;210&gt; 5

&lt;211&gt; 420

&lt;212&gt; PRT 3

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

```

Met Ile Ile Val Ala His Val Leu Leu Ile Leu Leu Gly Ala Thr Glu
 1           5           10           15
Ile Leu Gln Ala Asp Leu Leu Pro Asp Glu Lys Ile Ser Leu Leu Pro
          20           25           30
Pro Val Asn Phe Thr Ile Lys Val Thr Gly Leu Ala Gln Val Leu Leu
          35           40           45
Gln Trp Lys Pro Asn Pro Asp Gln Glu Gln Arg Asn Val Asn Leu Glu
          50           55           60
Tyr Gln Val Lys Ile Asn Ala Pro Lys Glu Asp Asp Tyr Glu Thr Arg
 65           70           75           80
Ile Thr Glu Ser Lys Cys Val Thr Ile Leu His Lys Gly Phe Ser Ala
          85           90           95
Ser Val Arg Thr Ile Leu Gln Asn Asp His Ser Leu Leu Ala Ser Ser
          100          105          110
Trp Ala Ser Ala Glu Leu His Ala Pro Pro Gly Ser Pro Gly Thr Ser
          115          120          125
Ile Val Asn Leu Thr Cys Thr Thr Asn Thr Thr Glu Asp Asn Tyr Ser
 130          135          140
Arg Leu Arg Ser Tyr Gln Val Ser Leu His Cys Thr Trp Leu Val Gly
 145          150          155          160
Thr Asp Ala Pro Glu Asp Thr Gln Tyr Phe Leu Tyr Tyr Arg Tyr Gly
          165          170          175
Ser Trp Thr Glu Glu Cys Gln Glu Tyr Ser Lys Asp Thr Leu Gly Arg
          180          185          190
Asn Ile Ala Cys Trp Phe Pro Arg Thr Phe Ile Leu Ser Lys Gly Arg
          195          200          205
Asp Trp Leu Ser Val Leu Val Asn Gly Ser Ser Lys His Ser Ala Ile
 210          215          220
Arg Pro Phe Asp Gln Leu Phe Ala Leu His Ala Ile Asp Gln Ile Asn
 225          230          235          240
Pro Pro Leu Asn Val Thr Ala Glu Ile Glu Gly Thr Arg Leu Ser Ile
          245          250          255
Gln Trp Glu Lys Pro Val Ser Ala Phe Pro Ile His Cys Phe Asp Tyr
          260          265          270
Glu Val Lys Ile His Asn Thr Arg Asn Gly Tyr Leu Gln Ile Glu Lys
          275          280          285
Leu Met Thr Asn Ala Phe Ile Ser Ile Ile Asp Asp Leu Ser Lys Tyr
          290          295          300
Asp Val Gln Val Arg Ala Ala Val Ser Ser Met Cys Arg Glu Ala Gly
 305          310          315          320
Leu Trp Ser Glu Trp Ser Gln Pro Ile Tyr Val Gly Asn Asp Glu His
          325          330          335
Lys Pro Leu Arg Glu Trp Phe Val Ile Val Ile Met Ala Thr Ile Cys
          340          345          350
Phe Ile Leu Leu Ile Leu Ser Leu Ile Cys Lys Ile Cys His Leu Trp
          355          360          365
Ile Lys Leu Phe Pro Pro Ile Pro Ala Pro Lys Ser Asn Ile Lys Asp
          370          375          380
Leu Phe Val Thr Thr Asn Tyr Glu Lys Ala Gly Ser Ser Glu Thr Glu
 385          390          395          400
Ile Glu Val Ile Cys Tyr Ile Glu Lys Pro Gly Val Glu Thr Leu Glu
          405          410          415
Asp Ser Val Phe
          420

```

<210> 6  
 <211> 424  
 <212> PRT 3  
 <213> Mus musculus

<400> 6

Met	Ala	Arg	Pro	Ala	Leu	Leu	Gly	Glu	Leu	Leu	Val	Leu	Leu	Leu	Trp
1				5					10					15	
Thr	Ala	Thr	Val	Gly	Gln	Val	Ala	Ala	Ala	Thr	Glu	Val	Gln	Pro	Pro
			20					25					30		
Val	Thr	Asn	Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Ile	Ile	Trp
		35					40					45			
Thr	Trp	Ser	Pro	Pro	Glu	Gly	Ala	Ser	Pro	Asn	Cys	Thr	Leu	Arg	Tyr
	50					55					60				
Phe	Ser	His	Phe	Asp	Asp	Gln	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu	Thr
65					70					75					80
His	Arg	Lys	Glu	Glu	Leu	Pro	Leu	Asp	Glu	Lys	Ile	Cys	Leu	Gln	Val
				85					90					95	
Gly	Ser	Gln	Cys	Ser	Ala	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Pro	Leu	Val
			100					105					110		
Lys	Lys	Cys	Ile	Ser	Pro	Pro	Glu	Gly	Asp	Arg	Glu	Ser	Ala	Val	Thr
		115					120					125			
Glu	Leu	Lys	Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Ser	Trp
	130					135					140				
Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	Asp	Thr	His	Tyr	Thr	Leu	Tyr	Tyr
145					150					155					160
Trp	Tyr	Ser	Ser	Leu	Glu	Lys	Ser	Arg	Gln	Cys	Glu	Asn	Ile	Tyr	Arg
			165						170					175	
Glu	Gly	Gln	His	Ile	Ala	Cys	Ser	Phe	Lys	Leu	Thr	Lys	Val	Glu	Pro
			180					185					190		
Ser	Phe	Glu	His	Gln	Asn	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	Ala	Gly
		195					200					205			
Lys	Ile	Arg	Pro	Ser	Cys	Lys	Ile	Val	Ser	Leu	Thr	Ser	Tyr	Val	Lys
	210					215					220				
Pro	Asp	Pro	Pro	His	Ile	Lys	His	Leu	Leu	Leu	Lys	Asn	Gly	Ala	Leu
225					230					235					240
Leu	Val	Gln	Trp	Lys	Asn	Pro	Gln	Asn	Phe	Arg	Ser	Arg	Cys	Leu	Thr
			245						250					255	
Tyr	Glu	Val	Glu	Val	Asn	Asn	Thr	Gln	Thr	Asp	Arg	His	Asn	Ile	Leu



260	265	270
Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met 275 280 285		
Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val 290 295 300		
Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp 305 310 315 320		
Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu 325 330 335		
Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe 340 345 350		
Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys 355 360 365		
Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu 370 375 380		
Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp 385 390 395 400		
Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val Leu Ile 405 410 415		
Glu Asn Leu Lys Lys Ala Ala Pro 420		

<210> 7  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 7

agaggaatta cccctggatg 20

<210> 8  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> anti-sense primer

<400> 8

tcaaggagct gctttcttca 20

<210> 9  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 9

gatccacttc ccaagaacag a 21

<210> 10  
 <211> 23  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 10

gatccggggcc cttttttttt ttt 23

<210> 11  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>

<223> VRCVTL is substituted for the 8 C-terminal amino acids of SEQ ID NO. 2 to give SEQ ID NO. 12

<400> 11  
 Val Arg Cys Val Thr Leu  
 1 5

<210> 12  
 <211> 378  
 <212> PRT 3  
 <213> Artificial sequence

<220>  
 <223> variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted for the 8 C-terminal amino acids of the human protein.

<400> 12

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile  
 1 5 10 15  
 Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val  
 20 25 30

```

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
   35                               40   45
Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
   50                               55   60
Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
   65                               70   75   80
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
   85                               90   95
Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
  100                               105  110
Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
  115                               120  125
Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
  130                               135  140
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
  145                               150  155  160
Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
  165                               170  175
Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
  180                               185  190
Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
  195                               200  205
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
  210                               215  220
Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
  225                               230  235  240
Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
  245                               250  255
Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
  260                               265  270
Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
  275                               280  285
Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
  290                               295  300
Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
  305                               310  315  320
Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
  325                               330  335
Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
  340                               345  350
Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
  355                               360  365
Tyr Pro Lys Met Val Arg Cys Val Thr Leu
  370                               375

```

<210> 13

<211> 5

<212> PRT 3

<213> Artificial sequence

<220>

<222> (1)...(5)

<223> motif characteristic of the family of chemokine receptors to which the polypeptides of SEQ ID NO. 2 and SEQ NO. 4 belong.

<223> Xaa can be any amino acid.

<400> 13

Trp Ser Xaa Trp Ser  
1 5

<210> 14

<211> 6

<212> DNA

<213> Artificial sequence

<220>

<223> polyadenylation signal

<400> 14

aataaaa 6

<210> 15

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 15

aaaaaaaaaa aaagggcccg 20